

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/538,038
Source: Pg 110
Date Processed by STIC: 6/16/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

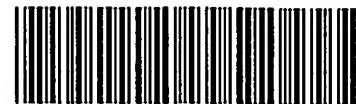
SUGGESTED CORRECTION

SERIAL NUMBER: 10/538,038

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/538,038

DATE: 06/16/2005

TIME: 10:24:46

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\06162005\J538038.raw

3 <110> APPLICANT: Givaudan SA
 5 <120> TITLE OF INVENTION: G-Proteins
 7 <130> FILE REFERENCE: 30069P1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/538,038
 C--> 9 <141> CURRENT FILING DATE: 2005-06-08
 9 <160> NUMBER OF SEQ ID NOS: 2
 11 <170> SOFTWARE: PatentIn version 3.1

IMPORTANT:
see item 4 on
Err summary sheet

pp 1-2

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1122
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (1)..(1122)
 21 <223> OTHER INFORMATION:
 W--> 23 <400> 1
 24 atg gcc cgc tgc acc tgg cgc tgc tgc ccc tgg tgc ctg acg gag 48
 E--> 26 1 5 10 15 96
 28 gat gag aag gcc gcc cgg gtg gac cag gag atc aac agg atc ctc 96
 E--> 30 20 25 30 144
 32 ttg gag cag aag aag cag gac cgc qqq gag ctg aag ctg ctt ttg 144
 E--> 34 35 40 45 192
 36 ggc cca gcc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc 192
 E--> 38 50 55 60 240
 40 atc cac gcc gcc ggc tgc gag gag gag cgc aag gcc ttc cgg ccc 240
 E--> 42 65 70 75 80 288
 44 ctg gtc tac cag aac atc ttc gtg tcc atg cgg gcc atg atc gag gcc 288
 E--> 46 85 90 95 336
 48 atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac 336
 E--> 50 100 105 110 384
 52 gct agc ctg gtc atg agc cag gac ccc tat aaa gtc acc acc ttt gag 384
 E--> 54 115 120 125 432
 56 aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc gcc atc 432
 E--> 58 130 135 140 480
 60 cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc 480
 E--> 62 145 150 155 160 528
 64 gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag gcc tac gtc 528
 E--> 66 165 170 175 576
 68 ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act gcc atc 576

Does Not Comply
Corrected Diskette Needed

Delete

numbers under codons.

Use numbers under every 5

amino

acids.

No

amino
acids

are
shown

in
this
sequence.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/538,038

DATE: 06/16/2005

TIME: 10:24:46

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\06162005\J538038.raw

```

E--> 70      180      185      190
72 aac gag tac tgc ttc tcc gtg cag aaa acc aac etg cgg atc gtg gac 624
E--> 74      195      200      205
76 gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag 672
E--> 78      210      215      220
80 aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag 720
E--> 82 225      230      235      240
84 tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca 768
E--> 86      245      250      255
88 ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc 816
E--> 90      260      265      270
94 atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc 864
E--> 96      275      280      285
98 tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat 912
E--> 100     290      295      300
102 gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac 960
E--> 104 305      310      315      320
106 acc ggg tgc gtg gac ggc ccc gag ggc agc aac tta aaa aaa gaa gat 1008
E--> 108     325      330      335
110 aag gaa atc tat tct cac atg acc tgc gct act gac aca caa aac gtc 1056
E--> 112     340      345      350
114 aaa ttc gtg ttt gat gcc gtg aca gat ata ata ata aaa gag aac ctc 1104
E--> 116     355      360      365
118 aaa gac tgt ggg ctc ttc 1122
E--> 120     370

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/538,038

DATE: 06/16/2005

TIME: 10:24:47

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\06162005\J538038.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:23 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21

L:26 M:254 E: No. of Bases conflict, this line has no nucleotides.

M:254 Repeated in SeqNo=1